10/500428
DT04 Rec'd PCT/PTO 28 JUN 2004

PATENT
Attorney Docket No. 229576
Client Reference No. 201213

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

SUGARU et al.

Application No. Unassigned

Filed: June 28, 2004

Art Unit: Unassigned

Examiner: Unassigned

For: REMEDIES FOR CIBOPHOBIA OR LIFESTYLE-RELATED DISEASES AND METHOD OF SCREENING THE SAME

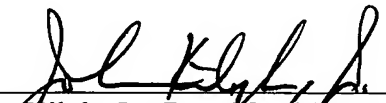
SUBMISSION OF SEQUENCE LISTING

Mail Stop PCT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

In accordance with the requirements of 37 CFR 1.821-1.825, a sequence listing is being submitted as part of the patent application. The sequence listing is in the form of both a paper copy and a computer readable copy on a computer diskette. The undersigned hereby verifies that the content of the paper copy and the computer readable copy, as concurrently being submitted, are the same.

Respectfully submitted,



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Date: June 28, 2004

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SEQUENCE LISTING

<110> Sumitomo Pharmaceuticals CO., LTD.

<120> Therapeutic Agent for Anorexia Nervosa or Life-Style Related Diseases, and Method for Screening Same

<130> 09517

<150> JP 2001-397523
<151> 2001-12-27

<160> 29

<170> PatentIn version 3.1

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<211> 1038
<212> RNA
<213> Homo sapiens

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<222> (1)..(1035)

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gac gcc gag ggg cca ugg ggc auc auu cug gag ucc cug gcc aua cuu      96
Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu
            20                  25                  30
ggc auc gug guc aca auu cug cua cuc uua gca uuu cuc uuc cuc aug     144
Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met
        35                  40                  45
cga aag auc caa gac ugc agc cag ugg aau guc cuc ccc acc cag cuc     192
Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu
    50                  55                  60
cuc uuc cuc cug agu guc cug ggg cuc uuc gga cuc gcu uuu gcc uuc     240
Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe
65                  70                  75                  80
auc auc gag cuc aau caa caa acu gcc ccc gua cgc uac uuu cuc uuu     288
Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
                85                  90                  95
ggg guu cuc uuu gcu cuc ugu uuc uca ugc cuc uua gcu cau gcc ucc     336
Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
            100                 105                 110
aau cua gug aag cug guu cgg ggu ugu guc ucc uuc ucc ugg acg aca     384
Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
        115                 120                 125
auu cug ugc auu gcu auu ggu ugc agu cug uug caa auc auu auu gcc     432
Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
    130                 135                 140
acu gag uau gug acu cuc auc aug acc aga ggu aug aug uuu gug aau     480
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Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
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aug aca ccc ugc cag cuc aau gug gac uuu guu gua cuc cug guc uau      528
Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
                165                 170                 175
guc cuc uuc cug aug gcc cuc aca uuc uuc guc ucc aaa gcc acc uuc      576
Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
            180                 185                 190
ugu ggc ccg ugu gag aac ugg aag cag cau gga agg cuc auc uuu auc      624
Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
        195                 200                 205
acu gug cuc uuc ucc auc auc auc ugg gug gug ugg auc ucc aug cuc      672
Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
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Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
225                 230                 235                 240
guc guc ugc auu gcu cug guc acc aac gca ugg guu uuc cug cug cug      768
Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
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uac auc guc ccu gag cuc ugc auu cuc uac aga ucg ugu aga cag gag      816
Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
            260                 265                 270
ugc ccu uua caa ggc aau gcc ugc ccc guc aca gcc uac caa cac agc      864
Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
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uuc caa gug gag aac cag gag cuc ucc aga gcc cga gac agu gau gga      912
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gcu gag gag gau gua gca uua acu uca uau ggu acu ccc auu cag ccg      960
Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
305                 310                 315                 320
cag acu guu gau ccc aca caa gag ugu uuc auc cca cag gcu aaa cua     1008
Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
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<212> PRT

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Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met
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Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
85 90 95

Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
100 105 110

Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
115 120 125

Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
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Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
145 150 155 160

Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
165 170 175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
180 185 190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
195 200 205

Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
210 215 220

Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
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Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
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Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
260 265 270

Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
275 280 285

Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
290 295 300

Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
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<222> (148)..(1047)

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ucucgugagg ucuaccuaua agucacc aug uau gag gac ugc gug aag ucc aca 174
Met Tyr Glu Asp Cys Val Lys Ser Thr
1 5

gaa gac uau uac cuc uuc ugu gac aac gag ggg cca ugg gcc auu guu 222
Glu Asp Tyr Tyr Leu Phe Cys Asp Asn Glu Gly Pro Trp Ala Ile Val
10 15 20 25

cug gag ucc uug gca gug auu ggc aua gug guu acc aua uug cua cuc 270
Leu Glu Ser Leu Ala Val Ile Gly Ile Val Val Thr Ile Leu Leu Leu
30 35 40

cug gca uuu cug uuc cuc aug cgg aag guu cag gac ugc agc cag ugg 318

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                45                  50                  55
aac gug cuu ccc acu cag uuc cuc uuc cug cug gcu gug cuc ggg cuc      366
Asn Val Leu Pro Thr Gln Phe Leu Phe Leu Leu Ala Val Leu Gly Leu
        60                  65                  70
uuc gga cuu acu uuu gcc uuc auc auc caa cuc aac cau caa acu gcc      414
Phe Gly Leu Thr Phe Ala Phe Ile Ile Gln Leu Asn His Gln Thr Ala
    75                  80                  85
ccu guu cgc uac uuc cuc uuu ggg guu cuc uuu gcu auc ugc uuc ucc      462
Pro Val Arg Tyr Phe Leu Phe Gly Val Leu Phe Ala Ile Cys Phe Ser
90                  95                  100                 105
ugc cuc cug gcu cau gcc ucc aac cug gug aag cug guc cgg ggu aga      510
Cys Leu Leu Ala His Ala Ser Asn Leu Val Lys Leu Val Arg Gly Arg
                110                 115                 120
guc ucc uuc ugc ugg aca aca auu cug uuc auu gcu auc ggu guc agc      558
Val Ser Phe Cys Trp Thr Thr Ile Leu Phe Ile Ala Ile Gly Val Ser
            125                 130                 135
cug uug cag acc auc auu gcg aua gag uau gug acc cuc auc aug acc      606
Leu Leu Gln Thr Ile Ile Ala Ile Glu Tyr Val Thr Leu Ile Met Thr
        140                 145                 150
aga ggc uug aug uuc gag cau aug aca ccg uau cag cuc aau gug gac      654
Arg Gly Leu Met Phe Glu His Met Thr Pro Tyr Gln Leu Asn Val Asp
    155                 160                 165
uuu guc ugu cuc cug auc uau guc cuc uuc cug aug gcc cuc acu uuc      702
Phe Val Cys Leu Leu Ile Tyr Val Leu Phe Leu Met Ala Leu Thr Phe
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uuc guc ucc aag gcc acc uuc ugu ggc cca ugu gag aac ugg aaa cag      750
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His Gly Arg Leu Ile Phe Ala Thr Val Leu Val Ser Ile Ile Ile Trp
            205                 210                 215

gug gug ugg auc ucc aug cuc uug aga ggc aac ccc cag cuc cag cga      846
Val Val Trp Ile Ser Met Leu Leu Arg Gly Asn Pro Gln Leu Gln Arg
        220                 225                 230

cag ccc cac ugg gac gau gca guc auc ugc auu ggc cug guc acc aac      894
Gln Pro His Trp Asp Asp Ala Val Ile Cys Ile Gly Leu Val Thr Asn
    235                 240                 245

gcu ugg guc uuc cug cug auc uac auc auc ccu gag cug agc aua cuc      942
Ala Trp Val Phe Leu Leu Ile Tyr Ile Ile Pro Glu Leu Ser Ile Leu
250                 255                 260                 265

uac agg uca ugu agg cag gag ugu ccu aca caa ggc aac guc ugc cag      990
Tyr Arg Ser Cys Arg Gln Glu Cys Pro Thr Gln Gly Asn Val Cys Gln
                270                 275                 280

guc ccu guc uac caa cgc agc uuc agg aug gau acc cag gaa ccc acc      1038
Val Pro Val Tyr Gln Arg Ser Phe Arg Met Asp Thr Gln Glu Pro Thr
            285                 290                 295
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aagcauccuu ccugucccuu ccucucuguu ucccugcccu uuccacucuu cuggacccag 1267

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35 40 45

Arg Lys Val Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Phe
50 55 60

Leu Phe Leu Leu Ala Val Leu Gly Leu Phe Gly Leu Thr Phe Ala Phe
65 70 75 80

Ile Ile Gln Leu Asn His Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
85 90 95

Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Leu Ala His Ala Ser
100 105 110

Asn Leu Val Lys Leu Val Arg Gly Arg Val Ser Phe Cys Trp Thr Thr
115 120 125

Ile Leu Phe Ile Ala Ile Gly Val Ser Leu Leu Gln Thr Ile Ile Ala
130 135 140

Ile Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Leu Met Phe Glu His
145 150 155 160

Met Thr Pro Tyr Gln Leu Asn Val Asp Phe Val Cys Leu Leu Ile Tyr
165 170 175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
180 185 190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ala
195 200 205

Thr Val Leu Val Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu
210 215 220

Leu Arg Gly Asn Pro Gln Leu Gln Arg Gln Pro His Trp Asp Asp Ala
225 230 235 240

Val Ile Cys Ile Gly Leu Val Thr Asn Ala Trp Val Phe Leu Leu Ile
245 250 255

Tyr Ile Ile Pro Glu Leu Ser Ile Leu Tyr Arg Ser Cys Arg Gln Glu
260 265 270

Cys Pro Thr Gln Gly Asn Val Cys Gln Val Pro Val Tyr Gln Arg Ser
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acctcttctg tgacaacgag 20

<210> 6

<211> 20

<212> DNA

<213> Artificial/Unknown

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<210> 7

<211> 25

<212> DNA

<213> Artificial/Unknown

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<210> 8

<211> 25

<212> DNA

<213> Artificial/Unknown

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<221> misc_feature

<223> Oligonucleotide designed to act as antisense DNA for sequence resulted from mutation causing abnormal splicing at position 705 of β-globin pre-mRNA in thalassemia.

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<210> 9

<211> 25

<212> DNA

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<211> 24

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<210> 12

<211> 23

<212> DNA

<213> Artificial/Unknown

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<223> Oligonucleotide designed to act as primer for amlifying GAPDH mRNA.

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<210> 13

<211> 20

<212> DNA

<213> Artificial

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<221> misc_feature

<223> Oligonucleotide designed to act as sense primer for amplifying human G protein Gα16 cDNA fragment containing full length ORF.

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<212> DNA

<213> Artificial

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<211> 19

<212> DNA

<213> Artificial

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<223> Oligonucleotide designed to act as sense primer for amplifying human G protein Gαi2 cDNA fragment containing full length ORF.

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<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

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<223> Oligonucleotide designed to act as antisense primer for amplifying human G protein Gαi2 cDNA fragment containing full length ORF.

<400> 16

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<210> 17

<211> 21

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as sense primer for amplifying human G protein GαS2 cDNA fragment containing full length ORF.

<400> 17

ccatgggctg cctcgggaac a 21

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as antisense primer for amplifying human G protein GαS2 cDNA fragment containng full length ORF.

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ggtttcgcaa aatcactcgg ggg 23

<210> 19

<211> 21

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as sense primer for amplifying human G protein Gα16 cDNA fragment from initiation codon.

<400> 19

atggcccgct cgctgacctg g 21

<210> 20

<211> 21

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as sense primer for amplifying human G protein Gαi2 cDNA fragment from initiation codon.

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<210> 21

<211> 20

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as sense primer for amplifying human G protein GαS2 cDNA fragment from initiation codon.

<400> 21

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<210> 22

<211> 18

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as antisense primer for amplifying multiple cloning site of plasmid pcDNA3.1(+).

<400> 22

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<210> 23

<211> 24

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Sense strand oligonucleotide designed to construct linker containing nucleotide sequence encoding 6xHis-tag peptide sequence.

<400> 23

gatatccatc atcatcatca ccat 24

<210> 24

<211> 18

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Antisense strand oligonucleotide desined to construct linker containing nucleotide sequence encoding 6xHis-tag peptide sequence.

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<210> 25

<211> 20

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as sence primer for amplifying GPRC5D cDNA.

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<210> 26

<211> 22

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as antisence primer for amplifying GPRC5D cDNA.

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<210> 27

<211> 58

<212> DNA

<213> Artificial

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<223> Oligonucleotide designed to act as sence primer for amplifying ORF of GPRC5D cDNA.

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<210> 28

<211> 55

<212> DNA

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<220>

<221> misc_feature

<223> Oligonucleotide designed to act as antisense primer for amplifying ORF (R form) of GPRC5D cDNA.

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<210> 29

<211> 51

<212> DNA

<213> Artificial

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<223> Oligonucleotide designed to act as antisense primer for amplifying ORF (F form) of GPRC5D cDNA.

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